

# SEQUENCE LISTING

<110> Kazuko, SHINOZAKI  
Mie, KASUGA

<120> Environmental Stress-Tolerant Plants

<130> 382.1029DIV1

<150> JP292348/1998  
US 09/301,217

<151> 1998-10-14  
1999-04-28

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<170> PatentIn Ver. 2.0

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atg aac tca ttt tct gct ttt tct gaa atg ttt ggc tcc gat tac gag 166  
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Glu Val Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp Leu Gly Thr Phe  
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caa acc gct gag atg gca gct cga gct cac gac gtt gcc gct tta gcc 406  
Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala  
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 Lys Arg Lys Ser Arg Ser Arg Gly Asp Gly Thr Thr Val Ala Glu Arg  
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Arg Gly Val Lys Ala Asp Lys His Trp Leu Ser Glu Phe Glu His Asn	
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gag act cgt cac cca att tac aga gga gtt cgt caa aga aac tcc ggt 314
Glu Thr Arg His Pro Ile Tyr Arg Gly Val Arg Gln Arg Asn Ser Gly
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Lys Trp Val Cys Glu Leu Arg Glu Pro Asn Lys Lys Thr Arg Ile Trp
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Ala Ala Ile Ala Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp
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Ser Ala Trp Arg Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Glu Ile
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Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Glu Ile Gln Lys Ala Ala
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Asp Ala His Gly Leu Asp Met Glu Glu Thr Leu Val Glu Ala Ile Tyr
145          150          155          160
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          20          25          30
aag tgg aaa gag tac aac gag att gtt gaa gct tcg gct gtt aaa gaa 323
Lys Trp Lys Glu Tyr Asn Glu Ile Val Glu Ala Ser Ala Val Lys Glu
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ccg aaa ata gga act aga ctt tgg ctt ggt act ttt cct acc gcg gaa			515
Pro Lys Ile Gly Thr Arg Leu Trp Leu Gly Thr Phe Pro Thr Ala Glu			
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tcctacaaga ctacaacata atctttggat tgatcatagg agaaacaaga aataggtggt			1252
aatgatctga ttcacaatga aaaaatattt aataactcta tagtttttgt tctttccttg			1312
gatcatgaac tgttgcttct catctattga gttaatatag cgaatagcag agtttctctc			1372

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tttttttctt ttgtagaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaayh sakmabgcar 1432
srcsdvsnaa nntnatnar sarchcntrr agrctrascn csrscaswash tskbabarak 1492
aantamaysa kmasrngnga c 1513

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<210> 10
<211> 330
<212> PRT
<213> Arabidopsis thaliana

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<400> 10
Met Ala Val Tyr Glu Gln Thr Gly Thr Glu Gln Pro Lys Lys Arg Lys
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Ser Arg Ala Arg Ala Gly Gly Leu Thr Val Ala Asp Arg Leu Lys Lys
 20          25          30
Trp Lys Glu Tyr Asn Glu Ile Val Glu Ala Ser Ala Val Lys Glu Gly
 35          40          45
Glu Lys Pro Lys Arg Lys Val Pro Ala Lys Gly Ser Lys Lys Gly Cys
 50          55          60
Met Lys Gly Lys Gly Gly Pro Asp Asn Ser His Cys Ser Phe Arg Gly
 65          70          75          80
Val Arg Gln Arg Ile Trp Gly Lys Trp Val Ala Glu Ile Arg Glu Pro
 85          90          95
Lys Ile Gly Thr Arg Leu Trp Leu Gly Thr Phe Pro Thr Ala Glu Lys
100          105          110
Ala Ala Ser Ala Tyr Asp Glu Ala Ala Thr Ala Met Tyr Gly Ser Leu
115          120          125
Ala Arg Leu Asn Phe Pro Gln Ser Val Gly Ser Glu Phe Thr Ser Thr
130          135          140
Ser Ser Gln Ser Glu Val Cys Thr Val Glu Asn Lys Ala Val Val Cys
145          150          155          160
Gly Asp Val Cys Val Lys His Glu Asp Thr Asp Cys Glu Ser Asn Pro
165          170          175
Phe Ser Gln Ile Leu Asp Val Arg Glu Glu Ser Cys Gly Thr Arg Pro
180          185          190
Asp Ser Cys Thr Val Gly His Gln Asp Met Asn Ser Ser Leu Asn Tyr
195          200          205
Asp Leu Leu Leu Glu Phe Glu Gln Gln Tyr Trp Gly Gln Val Leu Gln
210          215          220
Glu Lys Glu Lys Pro Lys Gln Glu Glu Glu Glu Ile Gln Gln Gln Gln
225          230          235          240
Gln Glu Gln Gln Gln Gln Gln Leu Gln Pro Asp Leu Leu Thr Val Ala
245          250          255
Asp Tyr Gly Trp Pro Trp Ser Asn Asp Ile Val Asn Asp Gln Thr Ser
260          265          270
Trp Asp Pro Asn Glu Cys Phe Asp Ile Asn Glu Leu Leu Gly Asp Leu
275          280          285
Asn Glu Pro Gly Pro His Gln Ser Gln Asp Gln Asn His Val Asn Ser
290          295          300
Gly Ser Tyr Asp Leu His Pro Leu His Leu Glu Pro His Asp Gly His
305          310          315          320
Glu Phe Asn Gly Leu Ser Ser Leu Asp Ile
325          330

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<210> 11
<211> 30
<212> DNA
<213> Artificial Sequence

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<220>  
 <223> Designed oligonucleotide based on the promoter region of rd29A gene and having HindIII site.

<400> 11  
 aagcttaagc ttacatcagt ttgaaagaaa 30

<210> 12  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Designed oligonucleotide based on the promoter region of rd29A gene and having HindIII site.

<400> 12  
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<210> 13  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Designed oligonucleotide based on DREB1A gene and having BamHI site.

<400> 13  
 aagcttaagc ttgccataga tgcaattcaa tc 32

<210> 14  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Designed oligonucleotide based on DREB1A gene and having BamHI site.

<400> 14  
 aagcttaagc ttttccaaag atttttttct ttccaa 36

<210> 15  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Designed oligonucleotide based on the promoter region of rd29A gene and having HindIII site.

<400> 15  
 ggatccgat ccatgaactc attttctgct 30

<210> 16

<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Designed oligonucleotide based on the promoter region of rd29A gene and having HindIII site.

<400> 16  
ggatccggat ccttaataac tccataacga ta 32

<210> 17  
<211> 941  
<212> DNA  
<213> Arabidopsis thaliana  
<400> 17

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gccatagatg caattcaatc aaactgaaat ttctgcaaga atctcaaaca cggagatctc 60
aaagtttgaa agaaaattta tttcttcgac tcaaaacaaa cttacgaaat ttaggtagaa 120
cttatataca ttatattgta attttttgta acaaaatggt tttattatta ttatagaatt 180
ttactgggta aattaaaaat gaatagaaaa ggtgaattaa gaggagagag gaggtaaaca 240
ttttcttcta ttttttcata ttttcaggat aaattattgt aaaagtttac aagatttcca 300
tttgactagt gtaaatgagg aatattctct agtaagatca ttatttcata tacttctttt 360
atcttctacc agtagaggaa taaacaatat ttagctcctt tgtaaataca aattaatttt 420
ccttcttgac atcattcaat ttttaatttta cgtataaaat aaaagatcat acctattaga 480
acgattaagg agaaatacaa ttcgaatgag aaggatgtgc cgtttggtat aataaacagc 540
cacacgacgt aaacgtaaaa tgaccacatg atgggccaat agacatggac cgactactaa 600
taatagtaag ttacatttta ggatggaata aatatcatal cgacatcagt tttgaaagaa 660
aagggaataa aagaaaaaat aaataaaaaga tatactaccg acatgagttc caaaaagcaa 720
aaaaaaaagat caagccgaca cagacacgcg tagagagcaa aatgactttg acgtcacacc 780
acgaaaacag acgcttcata cgtgtccctt tatctctctc agtctctcta taaacttagt 840
gagaccctcc tctgttttac tcacaaatat gcaaaactaga aaacaatcat caggaataaa 900
gggtttgatt acttctattg gaaagaaaaa aatctttgga a 941
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<210> 18  
<211> 71  
<212> DNA  
<213> Arabidopsis thaliana

<400> 18  
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ttccaaaaag c 71

<210> 19  
<211> 71  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide having a partially mutated sequence within the DRE region.

<400> 19  
cagtttgaaa gaaaagggaa aaaaagaaaa aataaataaa agatatattt tcgacatgag 60  
ttccaaaaag c 71

<210> 20  
<211> 71

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide having a partially mutated sequence within the DRE region.

<400> 20  
cagtttgaaa gaaaagggaa aaaaagaaaa aataaataaa agatatacta cttttatgag 60  
ttccaaaaag c 71

<210> 21  
<211> 71  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide having a partially mutated sequence within the DRE region.

<400> 21  
cagtttgaaa gaaaagggaa aaaaagaaaa aataaataaa agatatacta ccgacaaaag 60  
ttccaaaaag c 71

<210> 22  
<211> 71  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide having a partially mutated sequence outside the DRE region.

<400> 22  
cagtttgaaa gaaaagggaa aaaaagaaaa aataaataaa agatatacta ccgacatgat 60  
caacaaaaag c 71

<210> 23  
<211> 71  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide having a partially mutated sequence outside the DRE region.

<400> 23  
cagtttgaaa gaaaagggaa aaaaagaaaa aataaataaa agatatacta ccgacatgag 60  
ttcggttaag c 71